

SEQUENCE LISTING

<110> Pennica, Diane
Smith, Victoria
Wood, William I.

<120> Novel STRA6 Polypeptides

<13> GENENT, 2827A2

151-61197069
151-2000-04-14

(150-60) 75849
(151-2000-01-13)

(150) 60128914
(151) 2000-08-29

160

170 FastSEQ for Windows Version 4.0

4010-1
4011-2732
4012-DNA
4013-Homo Sapiens

4220
4221 CDS
4222 (49) . . . (2052)

<400°

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295

300

305

tac cag gtg gcc ctg ctg ctg gtg ggc gtg gta ccc act atc cag 1017
 Tyr Gln Val Ala Leu Leu Leu Val Gly Val Val Pro Thr Ile Gln
 310 315 320

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aag gtg agg gca ggg gtc acc acg gat gtc tcc tac ctg ctg gcc ggc 1066
Lys Val Arg Ala Gly Val Thr Thr Asp Val Ser Tyr Leu Leu Ala Gly
    325          330          335

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340 345 350 355

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aag cac cat ctg tgg gct ctg gaa gtg tgc tac atc tca gcc ttg gtc    lilel
Lys His His Ile Trp Ala Leu Glu Val Cys Tyr Ile Ser Ala Leu Val
            360          365          370

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ttg tcc tgc tta stc acc ttg ctg gtc ctg atg cgc tta ctg gtg aca 11289
Leu Ser Cys Leu Leu Thr Phe Leu Val Leu Met Arg Ser Leu Val Thr
      375          380          385

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cac agg acc aac ctt cga gct ctg cac cga gga gct gcc ctg gac ttg 1257
 His Arg Thr Asn Leu Arg Ala Leu His Arg Gly Ala Ala Leu Asp Leu
 390 395 400

agt ccc ttg cat cgg agt ccc cat ccc tcc cgg caa gcc ata ttc tgt 1305
 Ser Pro Leu His Arg Ser Pro His Pro Ser Arg Gln Ala Ile Phe Cys
 405 410 415

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tgg atg agc ttc agt gcc tac cag aca gcc ttt atc tgc ctt ggg ctc 1353
Trp Met Ser Phe Ser Ala Tyr Gln Thr Ala Phe Ile Cys Leu Gly Leu
420          425          430          435

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ctg gtg cag cag atc atc ttc ttc ctg gga acc acg gcc ctg gcc ttc 1401
 Leu Val Gln Gln Ile Ile Phe Phe Leu Gly Thr Thr Ala Leu Ala Phe
 440 445 450

Arg Ser Ser Trp Pro Ile Trp Leu Ile Leu Ala Leu Ala Val
422 423 424 425

and old hat ear at you and eat big his lots big gag air eat eat
the lion will eat me all his trip will the lion find the his help
and

1	5	10	15
Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gin Gly Gly Glu			
"	25	30	
Glu Leu Glu Ile Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Leu Pro			
"	40	45	
Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu			
50	55	60	
Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gin Leu Trp Pro Asp Cys			
65	70	75	80
Val Arg Gly Arg Pro Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly			
85	90	95	
Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe Met Val Leu Leu Ser			
100	105	110	
Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala Leu Pro Phe Leu Thr			
115	120	125	
Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr Glu Ala Pro Arg Gly			
130	135	140	
Ala Trp Lys Ile Leu Gly Leu Phe Tyr Tyr Ala Ala Leu Tyr Tyr Pro			
145	150	155	160
Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala Ala His Leu Leu Gly			
165	170	175	
Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln Val Trp Gln Arg Ala			
180	185	190	
Glu Cys Pro Gin Val Pro Lys Ile Tyr Lys Tyr Tyr Ser Leu Leu Ala			
195	200	205	
Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu Ser Leu Trp Tyr Pro			
210	215	220	
Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr Gly Ala Gly Ser Lys			
225	230	235	240
Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu Arg Asn Leu Leu Cys			
245	250	255	
Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser Lys His Gly Phe Leu			
260	265	270	
Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile Tyr Thr Pro Gln Pro			
275	280	285	
Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser Ala Thr Leu Thr Gly			
290	295	300	
Thr Ala Ile Tyr Gin Val Ala Leu Leu Leu Val Gly Val Val Pro			
"	"	"	320
Thr Ile Ile Ile Val Arg Ala Gly Val Thr Thr Asp Val Thr Tyr Ile			
"	"	"	330
Ile Ile Ile Ile Ile Ile Ile Val Ile Ile Ile Asp Ile Ile Ile Ile Val			
"	"	"	350
Ala Leu Val Ile His His Leu Trp Ala Leu Glu Val Cys Tyr Ile Ser			
355	360	365	
Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu Val Leu Met Arg Ser			
380	385	390	
Ile Val Ile His Arg Thr Asn Leu Arg Ala Ile His Arg Gly Ala Ala			
395	400	405	410

Leu	Phe	Arg	Ser	Leu	Glu	Ser	Ser	Trp	Pro	Phe	Trp	Leu	Thr	Ile	Ala	
465					470					475					480	
Leu	Ala	Val	Ile	Leu	Gln	Asn	Met	Ala	Ala	His	Trp	Val	Phe	Ile	Glu	
					485					490					495	
Thr	His	Asp	Gly	His	Pro	Gln	Leu	Thr	Asn	Arg	Arg	Val	Leu	Tyr	Ala	
					500				505					510		
Ala	Thr	Phe	Ile	Leu	Phe	Pro	Leu	Asn	Val	Leu	Val	Gly	Ala	Met	Val	
					515				520					525		
Ala	Thr	Trp	Arg	Val	Ile	Leu	Ser	Ala	Leu	Tyr	Asn	Ala	Ile	His	Leu	
					530				535					540		
Gly	Gln	Met	Asp	Leu	Ser	Leu	Leu	Pro	Pro	Arg	Ala	Ala	Thr	Leu	Asp	
545					550					555					560	
Pro	Gly	Tyr	Tyr	Thr	Tyr	Arg	Asn	Phe	Leu	Lys	Ile	Glu	Val	Ser	Gln	
					565					570					575	
Ser	His	Pr.	Ala	Met	Thr	Ala	Phe	Cys	Ser	Leu	Leu	Leu	Gln	Ala	Gln	
					580					585					590	
Ser	Ile	Leu	Leu	Pro	Arg	Thr	Met	Ala	Ala	Pro	Gln	Asp	Ser	Leu	Arg	Pro
					595					600					605	
Gly	Glu	Glu	Asp	Glu	Gly	Met	Gln	Leu	Ile	Gln	Thr	Lys	Asp	Ser	Met	
					610				615					620		
Ala	Lys	Gly	Ala	Arg	Pro	Gly	Ala	Ser	Arg	Gly	Arg	Ala	Arg	Trp	Gly	
625					630					635					640	
Leu	Ala	Tyr	Thr	Leu	Leu	His	Asn	Pro	Thr	Leu	Gln	Val	Phe	Arg	Lys	
					645					650					655	
Thr	Ala	Ile	Ile	Gly	Ala	Asn	Gly	Ala	Gln	Pro						
				660					665							

2210-3
2211-676
2212-DNA
2213-House

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<221> misc_feature
<222> (26)...(26)
<223> n = A, B, C or G

220

2210-008

<222> (186)...(2160)

400

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cccggtttgg gagcaacctg ttgcgttga gggacaagt tcggggagag atcaataaag 120
gaaaaggaaaag agacaaggaa gggagaggta aggagagagc ttgattggag gayaagggcc 180
agaga atg tcc tcc cag cca gca ggg aac cag acc tcc ccc ggg gcc aca 230
          Met Ser Ser Glu Pro Ala Gly Asn Cys Thr Ser Pro Gly Ala Thr

```

THE CITY OF ALEXANDRIA, VIRGINIA, IS LOCATED IN THE STATE OF VIRGINIA, AND IS A MUNICIPALITY.

1 5 10 15

gag gag tac tcc tat ggc agc tgg tac atc gat gag ccc caq ggg ggc 278
 Glu Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly
 20 25 30

gag gag ctc caa gca gag ggg gaa gtg ccc tcc tgc caa acc acc aqc ata 326
 Glu Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile
 35 40 45

cca tcc ggc ctg taa cac gcc tgc ctg gcc tgg ctg tca atc ctt gtg 374
 Pro Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val
 50 55 60

ctg ctg ctc ctg gct atg ctg gtg agg cgc cgc cag ctc tgg cct gag 422
Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp
65 70 75

tgt gtg cgt ggc agg ccc ggc ctg ccc agg ccc cgg gca gtg cct gct 470
 Cys Val Arg Gly Arg Pro Gly Leu Pro Arg Pro Arg Ala Val Pro Ala
 29 35 39 43 47 51 55 59 63 67 71 75 79 83

gct gtt ttc atg gtc ctc ctg agc tcc ctg tgt ttg ctg ctc ccc gag 518
 Ala Val Phe Met Val Leu Ileu Ser Ser Leu Cys Leu Leu Ileu Pro Asp
 123 165 170

gag gac gca ttg ccc ttc ctg act ctc gcc tca gca ccc agc caa gat 566
Glu Asp Ala Leu Pro Phe Ieu Thr Leu Ala Ser Ala Prc Ser Gin Asp

Tat Tat Gln Ile Ser Thr Val Asp Glu Gln Lys Gln Arg Ile Ile
 Tyr Tyr Ala Leu Tyr Tyr Pro Leu Ala Ala Cys Ala Thr Ala Gly

Las actividades de las Naciones Unidas en el campo de la cultura y la ciencia.

Tyr Lys Tyr Tyr Ser Leu Leu Ala Ser Leu Pro Leu Leu Leu Gly Leu			
195	200	205	
gga ttc ctg aca ctt tgg tac cct gtg cag ctg gtg aca aca ttc aca			254
Gly Phe Leu Ser Leu Trp Tyr Pro Val Gln Leu Val Arg Ser Phe Ser			
210	215	220	
cgt agg aca gga gca ggc tcc aac ggg ctg cag aca aca tac tat gag			257
Arg Arg Thr Gly Ala Gly Ser Lys Gly Leu Gln Ser Ser Tyr Ser Glu			
225	230	235	
gaa tat ctg agg aac ttc ctt tgg agg aac aac ctg gca aca aca tac			261
Glu Tyr Leu Arg Asn Leu Leu Cys Arg Lys Lys Leu Gly Ser Ser Tyr			
240	245	250	255
cac acc tcc aag cat ggc ttc ctg tcc tgg gcc cgc gtc tgc ttg aga			298
His Thr Ser Lys His Gly Phe Leu Ser Trp Ala Arg Val Cys Leu Arg			
260	265	270	
cac tcc atc tac act cca cag cca gga ttc cat ctc ccg ctg aac ctg			1046
His Cys Ile Tyr Thr Pro Gln Pro Gly Phe His Leu Pro Leu Lys Leu			
275	280	285	
gtg ctt tca gct aca ctg aca ggg acg gcc att tac caa gtg gca ctg			1094
Val Leu Ser Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu			
290	295	300	
ctg ctg ctg ggc gtg gta ccc act atc cag aac gtg agg gca ggg			1142
Ile Leu Leu Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly			
305	310	315	
gtc acc aca gat gtc tcc tac ctg ctg gcc ggc ttt gga atc gtg ctc			1190
Val Thr Thr Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu			
320	325	330	335
tcc gag gag aac cag gag gtg gtg cag ctg gtg aac cac cat ctg tgg			1237
Ser Glu Asp Lys Gln Glu Val Val Glu Leu Val Lys His His Leu Trp			
340	345	350	
atc ttt			1254
Ala Leu Leu Val Tyr Dyp			
355	360	365	
acc ttc ttt gtc ttt aca aca ttt aca ttt gtc aca cat aac aac aac			1264
Thr Phe Leu Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu			
370	375	380	
atc ttt			1274
Ala Leu Leu Val Asp			
385	390	395	

420	425	430	
atc ttc ttc ctg gga acc acg gcc ctg gcc ttc ctg gtg cts atg cct Ile Phe Phe Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro			1516
435	440	445	
gtg ctc cat ggc agg aac ctc ctg ctc ttc cgt tcc ctg gag tcc tcg Val Leu His Gly Arg Asn Leu Leu Phe Arg Ser Leu Glu Ser Ser			1574
450	455	460	
tgg ccc ttc tgg ctg act ttg gcc ctg gct gtg atc ctg cag aac atg Trp Pro Phe Trp Leu Thr Leu Ala Leu Ala Val Ile Leu Gln Asn Met			1622
465	470	475	
gca gcc cat tgg gtc ttc ctg gag act cat gat gga cac cca cag ctg Ala Ala His Trp Val Phe Leu Glu Thr His Asp Gly His Pro Gln Leu			1670
480	485	490	495
acc aac cgg cga gtg ctc tat gca gcc acc ttt ctt ctc ttc ccc ctc Thr Asn Arg Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu			1718
500	505	510	
aat gtg ctg gtg ggt gcc ata gtc gcc acc tgg cga gtg ctc ctc tct Asn Val Leu Val Gly Ala Ile Val Ala Thr Trp Arg Val Leu Leu Ser			1766
515	520	525	
gcc ctc tac aat gcc atc cac ctt ggc cag atg gac ctc agc ctg ctg Ala Leu Tyr Asn Ala Ile His Leu Glu Gln Met Asp Leu Ser Leu Leu			1814
530	535	540	
ccs ccc aga gcc gcc act ctc gac ccc ggc tac tac acg tac cga aac Pro Pro Arg Ala Ala Thr Leu Asp Pro Gly Tyr Tyr Thr Arg Asn			1862
545	550	555	
ttc ttc aag att caa gtc agc cag tgg cat cca gcc atg aca gca ttc Phe Leu Lys Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe			1910
560	565	570	575
*** End of sequence ***			
ttt ttt Ala Pro Gln Asp Ser Leu Arg Pro Gly Glu Glu Asp Glu Gly Met Gln			1914
585	600	605	
ttg cta ttt ttt ttt gac ttt atg gcc aag ttt gtt agg ctt gtt gcc Leu Leu Lys Thr Tyr Asp Ser Met Ala Lys Ala Arg Ile Gly Ala			1918
610	615	620	

gcc caa ttt gggccaggg gaggtcaacc cactgcca tctgtgtt ja
Ala Gln Ile

211

ggcatgttc tgcataacc ctcccccctc cccggctctc ctccccat cacaccagcc 2260
atgcagedcg tgggtctctc ggtactgtt gtgtgggtgg aggtctgttc gcactggag 2320
atccagjajj jctctgttcc accacttgg ctatggaga gccagcaggg gttctggaga 2380
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ugggjt ttttttttttttttggcactt ccacctcage ctggcccttc acgctgtggg agcagccaaq 2500
gcacccatcc atccatcag cggcacggac ctctctgggg aatggccggg aagctcccgj 2560
jcccttgg tccaggcag ccacagtcat gactcagacc aggtccccaca ctqagctgca 2620
ccacatcgg agccagatat ttttgtatit tttatgtt tggctattat gaaagaggtt 2680
atgtgtgtttt atgcaataaa cttgttccgt agaaaaaa 2740

2777

210 - 5

211 - 658

212 - FRT

213 - Homo sapiens

2400 - 5

Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr Glu
1 5 10 15
Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly Glu
20 25 30
Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Pro
35 40 45
Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu
50 55 60
Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp Cys
65 70 75 80
Val Arg Gly Arg Pro Gly Leu Pro Arg Pro Arg Ala Val Pro Ala Ala
85 90 95
Val Phe Met Val Leu Leu Ser Ser Leu Cys Leu Leu Leu Pro Asp Glu
100 105 110
Asp Ala Leu Ile Phe Leu Thr Leu Ala Ser Ala Pro Ser Gln Asp Gly
115 120 125
Lys Thr Val Aln Phe Asn Gly Ala Trp Lys Ile Leu Gly Leu Ile Tyr
130 135 140
Tyr Ala Val Ile Tyr Tyr Ile Val Aln Ala Thr Ala Gly His
145 150 155 160
Thr Ala Val His Ile Ile Tyr Ser Thr Leu Ser Trp Ala His Leu Gly
165 170 175 180
Val Gln Val Trp Gln Arg Ala Glu Cys Pro Gln Val Pro Lys Ile Tyr
185 190 195 200
Lys Tyr Tyr Ser Leu Leu Ala Ser Leu Pro Leu Leu Gly Leu Gly
205 210 215 220
Ile Leu Ser Ile Ile Tyr Ile Val Phe Leu Val Arg; Tyr Ile Ile Arg

278	280	285
Leu Ser Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu Leu		
290	295	300
Leu Leu Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly Val		
305	310	315
Thr Thr Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu Ser		
325	330	335
Glu Asp Lys Gln Glu Val Val Glu Leu Val Lys His His Leu Trp Ala		
340	345	350
Leu Glu Val Lys Tyr Ile Ser Ala Leu Val Leu Ser Cys Leu Leu Thr		
355	360	365
Phe Leu Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu Arg		
370	375	380
Ala Leu His Arg Gly Ala Ala Leu Asp Leu Ser Pro Leu His Arg Ser		
385	390	395
Pro His Pro Ser Arg Gln Ala Ile Phe Cys Trp Met Ser Phe Ser Ala		
405	410	415
Tyr Gln Thr Ala Phe Ile Cys Leu Gly Leu Leu Val Gln Gln Ile Ile		
420	425	430
Phe Phe Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro Val		
435	440	445
Leu His Gly Arg Asn Leu Leu Leu Phe Arg Ser Leu Glu Ser Ser Trp		
450	455	460
Pro Phe Trp Leu Thr Leu Ala Leu Ala Val Ile Leu Gln Asn Met Ala		
465	470	475
480		
Ala His Trp Val Phe Leu Glu Thr His Asp Gly His Pro Gln Leu Thr		
485	490	495
Asn Arg Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn		
500	505	510
Val Leu Val Gly Ala Ile Val Ala Thr Trp Arg Val Leu Leu Ser Ala		
515	520	525
Leu Tyr Asn Ala Ile His Leu Gly Gln Met Asp Leu Ser Leu Leu Pro		
530	535	540
Pro Arg Ala Ala Thr Leu Asp Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe		
545	550	555
560		
Leu Lys Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe Cys		
565	570	575
Ser Leu Leu Leu Gln Ala Gln Ser Leu Leu Pro Arg Thr Met Ala Ala		
580	585	590
Pro Gln Asp Thr Leu Asn Ser Gly Thr Val Asp Gln Gln Met Gln Ile		
595	600	605
Leu Gln Val Lys Asp Thr Met Ala Lys Gly Ala Arg Ile Gly Asn Val		
610	615	620
Arg Gly Arg Ala Arg Trp Gly Leu Ala Tyr Thr Leu Leu His Asn Pro		
625	630	635
640		
Thr Leu Ile Val Phe Arg Lys Thr Ala Leu Leu Gly Ala Asn Gly Ala		
645	650	655
660		